

## RESULT 5

A26054

asparaginase (EC 3.5.1.1) precursor - *Erwinia chrysanthemi*C:Species: *Erwinia chrysanthemi*

C&gt;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 31-Dec-2004

C:Accession: A26054; S03681

R:Minton, N.P.; Bullman, H.M.S.; Scawen, M.D.; Atkinson, T.; Gilbert, H.J.

Gene 46, 25-35, 1986

A:Title: Nucleotide sequence of the *Erwinia chrysanthemi* NCPPB 1066 L-asparaginase

gene.

A:Reference number: A26054; MUID:87106840; PMID:3026924

A:Accession: A26054

A:Molecule type: DNA

A:Residues: 1-348 &lt;MIN&gt;

A:Cross-references: UNIPROT:P06608; UNIPARC:UPI000002C8D8; GB:M14741; GB:X14777;

NID:g42965; PIDN:CAA32884.1; FID:g4185897

A&gt;Note: the authors translated the codon AAG for residue 286 as Leu

R:Filpula, D.; Nagle, J.W.; Pulford, S.; Anderson, D.M.

Nucleic Acids Res. 16, 10385, 1988

A:Title: Sequence of L-asparaginase gene from *Erwinia chrysanthemi* NCPPB 1125.

A:Reference number: S03681; MUID:89057497; PMID:3194219

A:Accession: S03681

A&gt;Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-176, 'I', 178-198, 'R', 200-287, 'L', 289-294, 'M', 296-348 &lt;FIL&gt;

A:Cross-references: UNIPARC:UPI000016BE0D; GB:X12746; NID:g40993; PIDN:CAA31239.1;

FID:g40994

C:Superfamily: L-asparaginase/Glutamyl-tRNA (Gln) amidotransferase subunit D

C:Keywords: hydrolase

F:1-21/Domain: signal sequence #status predicted &lt;SIG&gt;

F:22-348/Product: asparaginase #status predicted &lt;MAT&gt;

Query Match 38.0%; Score 716; DB 1; Length 348;  
 Best Local Similarity 46.7%; Pred. No. 1.9e-40;  
 Matches 163; Conservative 59; Mismatches 103; Indels 24; Gaps 8;

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Qy      30  FVFTNANGLNFTQMNTTLPNVTIFATGGTIGAGSDSSSTATTGYTSAGVGLSLIDAVPSM  89
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      15  FVFT-----ASAADKLPNIVILATGGTIGAGSAATGTQTTGYKAGALGVDTLINAVPEV  67

Qy      90  LDVANVAGVQVANVGSSEDITSILISMSKKLNRVVCEDEPTMAGAVITHGTDLTLEETAFFL  149
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      68  KKLAVNKGEQFSNMASENMTGDVVLKLSQRVNEELLARD-DVDGVVITHGTDLTREASAYFL  126

Qy     150  DATVNCGKPIVIVGMRRPSTAISADGPPNLLRAVTAASTSARDRGMMVMNDRIASAYY  209
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db     127  HLTYSKDKPVVFVAAAMRPATAISADGPPNLLRAVVRVAGDKQSRGRGVMVVLNDRIGSARY  186

Qy     210  VTIKNTANTMDTFICAMEMGYLGEMISNTPFFFPYVK-PTGKVAFDITNVEIPRVDIIFS  268
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db     187  IYTKNASTLDTFCAMEEGYLOVIGNRIYQNRIDKLHTRSVFDVRGLTSLPKVDILYG  246

Qy     269  YEDMHNHTLYN-AISSGAQGIIVAGAGAGGVT---TSFNEAIEDVINRLEIPVQSMRT  323
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db     247  YQD-DEPYLYDAAIQHGKGIYVAGMGAGSVSVRGIAIGMRKAMEK-----GVVIRSTRK  300

Qy     324  VNGEVLPLSDVSSDTATHIASGVLPQKSRILLGLLLSQGNITRIADVF  372
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db     301  QNGIVP-----PDEELPGLVSDSLNPAHARILLMLALTRTSDPKVIQYEF  345

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